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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=6; hr=14; min=22; sec=50; ms=92;]

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Application No: 10522106 Version No: 3.0

Input Set:

Output Set:

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Started:      2009-12-15 16:22:28.242
Finished:    2009-12-15 16:22:35.214
Elapsed:      0 hr(s) 0 min(s) 6 sec(s) 972 ms
Total Warnings: 14
Total Errors:  66
No. of SeqIDs Defined: 36
Actual SeqID Count: 36

```

[illegible]

Input Set:

Output Set:

Started: 2009-12-15 16:22:28.242
Finished: 2009-12-15 16:22:35.214
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 972 ms
Total Warnings: 14
Total Errors: 66
No. of SeqIDs Defined: 36
Actual SeqID Count: 36

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (17)
E 300	Invalid codon found Thr SEQID (17) POS: 1153
E 300	Invalid codon found Ala SEQID (17) POS: 1156
E 300	Invalid codon found Val SEQID (17) POS: 1159
E 300	Invalid codon found His SEQID (17) POS: 1162
E 300	Invalid codon found Thr SEQID (17) POS: 1165
E 300	Invalid codon found Leu SEQID (17) POS: 1168
E 300	Invalid codon found Ala SEQID (17) POS: 1171
E 300	Invalid codon found His SEQID (17) POS: 1174
E 300	Invalid codon found Val SEQID (17) POS: 1177
E 300	Invalid codon found Thr SEQID (17) POS: 1180
E 300	Invalid codon found Cys SEQID (17) POS: 1183
E 300	Invalid codon found Asp SEQID (17) POS: 1186
E 300	Invalid codon found Phe SEQID (17) POS: 1189
E 300	Invalid codon found Pro SEQID (17) POS: 1192
E 300	Invalid codon found Arg SEQID (17) POS: 1195
E 300	Invalid codon found Leu SEQID (17) POS: 1198
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)

Input Set:

Output Set:

Started: 2009-12-15 16:22:28.242
Finished: 2009-12-15 16:22:35.214
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 972 ms
Total Warnings: 14
Total Errors: 66
No. of SeqIDs Defined: 36
Actual SeqID Count: 36

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
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W 213	Artificial or Unknown found in <213> in SEQ ID (33)
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SEQUENCE LISTING

<110> Kogel, Karl-Heinz
Huckelhoven, Ralph
Trujillo, Marco

<120> Method for Obtaining a Pathogen Resistance in Plants

<130> 12810-00067-US

<140> 10522106

<141> 2009-12-15

<150> PCT/EP03/07589

<151> 2003-07-14

<150> DE 10233327.0

<151> 2002-07-22

<160> 36

<170> PatentIn Ver. 3.3

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<211> 337

<212> DNA

<213> Hordeum vulgare

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<221> CDS

<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

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5

10

15

att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct 97

Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala

20

25

30

cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145

Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn

35

40

45

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Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg

50

55

60

cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241

Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr

65

70

75

80

gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa 289

Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu

85

90

95

cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337

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105

110

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<213> Hordeum vulgare

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20 25 30
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35 40 45
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
50 55 60
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
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<223> coding for NADPH oxidase

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Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp
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Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp
35 40 45
ctg cag gac gac gac acc att gtg ctt cgg agc gtc gag ccc gcg gcg 192
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala
50 55 60
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Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg
65 70 75 80
ggg gag ctc acg ggt ggc ccg tcg tcg tcg tcg tcg cgg tcg agg tcg 288
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Ser Arg Ser Arg Ser
85 90 95
ccg tcg atc cgg agg agc tcg tcg cac cgg ctg ctg cag ttc tcg cag 336
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln
100 105 110
gag ctc aag gcg gag gcc atg gcc cgg gcg cgg cag ttc tcg cag gac 384

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Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	
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Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala	
		210				215					220					
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Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp	
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acg	att	aac	aag	gat	gaa	ctc	cgc	gag	atc	tgg	cag	cag	atc	acc	gat	768
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			245					250					255			
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Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys	
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Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met	
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Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	
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Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly	
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Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr	
			325					330					335			
tat	atg	aac	tat	agt	cag	gcc	ctt	agt	tac	aca	agc	caa	gca	ctg	agc	1056
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	
		340					345					350				
cag	aat	ctt	gca	ggg	cta	agg	aag	aag	agt	tca	atc	cgc	aaa	ata	agc	1104
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser	
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Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val	
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Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	
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Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr	
			435				440					445				
agg	gct	gca	cgg	gca	cta	cct	ttt	gat	gac	aac	atc	aac	ttc	cac	aag	1392
Arg	Ala	Ala	Arg	Ala	Leu	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	
			450				455				460					
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Thr	Ile	Ala	Ala	Ala	Ile	Val	Val	Gly	Ile	Ile	Leu	His	Ala	Gly	Asn	
						470				475					480	
cac	ctt	gta	tgc	gat	ttt	cca	cgg	tta	ata	aaa	tca	tca	gat	gag	aag	1488
His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Lys	Ser	Ser	Asp	Glu	Lys	
				485					490					495		
tat	gct	cct	ttg	ggc	cag	tat	ttt	ggg	gaa	ata	aag	cca	aca	tat	ttt	1536
Tyr	Ala	Pro	Leu	Gly	Gln	Tyr	Phe	Gly	Glu	Ile	Lys	Pro	Thr	Tyr	Phe	
			500					505					510			
aca	ttg	gtc	aaa	gga	gtg	gag	ggc	atc	act	ggg	gta	atc	atg	gtt	gta	1584
Thr	Leu	Val	Lys	Gly	Val	Glu	Gly	Ile	Thr	Gly	Val	Ile	Met	Val	Val	
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tgc	atg	ata	att	gct	ttt	act	cta	gca	acc	cgg	tgg	ttc	cgc	cgt	agc	1632
Cys	Met	Ile	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser	
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Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ile	Ala	Leu	Ile	
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aca	tgg	atg	tat	ctt	tca	gtg	cct	gtt	tgc	ttg	tat	gta	ggg	gag	agg	1824
Thr	Trp	Met	Tyr	Leu	Ser	Val	Pro	Val	Cys	Leu	Tyr	Val	Gly	Glu	Arg	
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Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile		
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Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu		
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caa	gct	ctg	aac	cat	gcc	aag	aat	gga	gtt	gat	att	gtc	tct	ggg	aca	2640	
Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr		
			865				870			875				880			
aaa	gtc	cgg	aca	cat	ttt	gca	cga	cca	aat	tgg	aga	aag	gtc	ctt	tct	2688	
Lys	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Leu	Ser		
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aaa	att	tcc	tcc	aag	cat	cca	tat	gcc	aaa	ata	ggg	gta	ttc	tac	tgt	2736	
Lys	Ile	Ser	Ser	Lys	His	Pro	Tyr	Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys		
			900					905				910					
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Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu	Leu	Ser	Lys	Leu	Cys	His	Glu	Phe		
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 <212> PRT
 <213> Oryza sativa

<400> 4

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			20					25					30				
Asp	Arg	Ser	Ser	Asp	Asp	Gly	Glu	Glu	Leu	Val	Glu	Val	Thr	Leu	Asp		
			35				40					45					
Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala	Ala		
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Ala	Ala	Ala	Ala	Gly	Val	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Arg	65	70	75	80
Gly	Glu	Leu	Thr	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Arg	Ser	85	90	95	
Pro	Ser	Ile	Arg	Arg	Ser	Ser	Ser	His	Arg	Leu	Leu	Gln	Phe	Ser	Gln	100	105	110	
Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	115	120	125	
Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	130	135	140	
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	145	150	155	160
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg	165	170	175	
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu	180	185	190	
Val	Gln	Ala	Asn	Phe	Asp	Arg	Leu	Ala	Arg	Asp	Gly	Tyr	Leu	Ser	Arg	195	200	205	
Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala	210	215	220	
Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp	225	230	235	240
Thr	Ile	Asn	Lys	Asp	Glu	Leu	Arg	Glu	Ile	Trp	Gln	Gln	Ile	Thr	Asp	245	250	255	
Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys	260	265	270	
Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met	275	280	285	
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	290			